

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:)
)
Salvatore Albani)
)
Serial No: Not yet assigned)
)
Filed: Herewith)
)
For: METHODS FOR ISOLATION,)
QUANTIFICATION, CHARACTERIZATION)
AND MODULATION OF ANTIGEN-SPECIFIC T)
CELLS)

SUBMISSION OF SEQUENCE LISTING

Commissioner for Patents
Washington, D.C. 20231

Sir:

Applicants submit herewith the "Sequence Listing" in paper copy and in computer readable form as required under § 1.824 (a).

The Sequence Listing is provided in ASCII text on the accompanying diskette and the Statement Under 37 C.F. R. § 1.821 (f) is also provided.

Please amend the specification by entering the enclosed Sequence Listing. The Sequence Listing was generated from the specification and figures.

CERTIFICATE OF MAILING
(37 C.F.R. §1.8a)

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Respectfully submitted,

Brobeck, Phleger & Harrison LLP

Dated: 1/19/07

By 

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<210> 3
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized peptide derived from the hemophilus
 influenza virus

<400> 3
 Thr Ser Phe Pro Met Arg Gly Asp Leu Ala Lys Arg Glu Pro Asp Lys
 1 5 10 15

<210> 4
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized peptide derived from the TCR receptor
 gene of Mus musculus

<400> 4
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 Ser Gln Glu Phe Phe Ser Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr
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 Arg Leu
 35

<210> 5
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized peptide derived from the influenza virus

<400> 5
 Gly Ile Leu Gly Phe Val Phe Thr Leu
 1 5

<210> 6
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized peptide derived from the influenza virus

<400> 6
 Val Lys Leu Gly Glu Phe Tyr Asn Gln
 1 5

0075693-010601

<210> 7
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized peptide totally artificial

<220>
 <223> Xaa in position 2 stands for cyclohexylalanine

<400> 7
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 1 5 10

<210> 8
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized peptide derived from the influenza virus

<400> 8
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 1 5 10

<210> 9
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized peptide derived from the ovalbumin
 of Mus musculus

<400> 9
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 1 5 10 15
 Arg

<210> 10
 <211> 15
 <212> PRT
 <213> E. coli

<220>
 <223> dnaJpl heat shock protein

<400> 10
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 1 5 10 15

09756983-010901

<210> 11
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 11
 Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly
 1 5 10 15

<210> 12
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 12
 Gly Ile Leu Gly Phe Val Phe Thr Leu
 1 5

<210> 13
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 13
 Val Lys Leu Gly Glu Phe Tyr Asn Gln
 1 5

<210> 14
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 14
 Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
 1 5 10

<210> 15
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion constructs with human and bacterial sequences

<400> 15
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 20 25 30
 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu

0375693.0394
 "05070" 0375693.0394

35 40 45
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 50 55 60
 Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
 65 70 75 80
 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
 85 90 95
 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
 100 105 110
 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
 115 120 125
 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
 130 135 140
 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
 145 150 155 160
 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
 165 170 175
 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
 180 185 190
 Pro Glu Thr Glu Leu Tyr Ala Val Ser Glu Phe Gly Gly Ser Gly Gly
 195 200 205
 Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu Tyr His Asn
 210 215 220
 Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr Thr Glu Ser
 225 230 235 240
 Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala
 245 250 255
 Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys
 260 265 270
 Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala Tyr Leu Thr
 275 280 285
 Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys Thr Pro His
 290 295 300
 Ala Ile Ala Ala Ile Ser Met Ala Asn
 305 310

<210> 16

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

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 atttgcctaa cctctggagg tttccagag cctcacctct cctggttgga aaatggagaa 540
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 ctagctggaa aaagagagat ggctatcatt actttttaaga atgggtgcaac ttttcaagta 780
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<210> 17

<211> 1056

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

<400> 17

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 aaccaaagcc tgagtgaact agtagtattt tggcaggacc aggaaaactt ggttctgaat 180
 gaggtatact taggcaaaga gaaatttgac agtggttcatt ccaagtatat gggccgcaca 240
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 ttgtatcaat gtatcatcca tcacaaaaag cccacaggaa tgattcgcac ccaccagatg 360
 aattctgaac tgtcagtgct tgctaacttc agtcaacctg aaatagtacc aatttctaata 420
 ataacagaaa atgtgtacat aaatttgacc tgctcatcta tacacgggta cccagaacct 480
 aagaagatga gtgttttgc aagaaccaag aattcaacta tcgagtatga tggattatg 540
 cagaaatctc aagataatgt cacagaactg tacgacgtt ccatcagctt gtctgtttca 600
 ttccctgatg ttacgagcaa tatgaccatc ttctgtattc tggaaactga caagacgcgg 660
 cttttatctt cacccttctc tatagagctt gaggaccctc agcctcccc agaccacgaa 720
 ttcgggcggt cgggtggtag cgccacacct caaaatatta ctgatttgtg tgcagaatac 780
 cacaacacac aaatacatat gctaaatgat aagatatttt cgtatacaga atctctagct 840
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<210> 18

<211> 351

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

<400> 18

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Ala	Ala	Pro	Leu	Lys	Ile	Gln	Ala	Tyr	Phe	Asn	Glu	Thr	Ala	Asp	Leu
			20					25					30		
Pro	Cys	Gln	Phe	Ala	Asn	Ser	Gln	Asn	Gln	Ser	Leu	Ser	Glu	Leu	Val
			35				40					45			
Val	Phe	Trp	Gln	Asp	Gln	Glu	Asn	Leu	Val	Leu	Asn	Glu	Val	Tyr	Leu
			50			55					60				
Gly	Lys	Glu	Lys	Phe	Asp	Ser	Val	His	Ser	Lys	Tyr	Met	Gly	Arg	Thr
65					70				75					80	
Ser	Phe	Asp	Ser	Asp	Ser	Trp	Thr	Leu	Arg	Leu	His	Asn	Leu	Gln	Ile
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<210> 19
<211> 31
<212> PRT
<213> Artificial Sequence
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20 25 30

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<400> 22
Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
 1             5             10             15
Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
      20             25             30

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Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
 35 40 45
 Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
 50 55 60
 Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
 65 70 75 80
 Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
 85 90 95
 Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
 100 105 110
 Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
 115 120 125
 Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
 130 135 140
 Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
 145 150 155 160
 Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
 165 170 175
 Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
 180 185 190
 Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
 195 200 205
 Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser
 210 215 220
 Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln
 225 230 235 240
 Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly
 245 250 255
 Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu
 260 265 270
 Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr
 275 280 285
 Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys
 290 295 300
 Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
 305 310 315 320
 Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala
 325 330 335
 Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys
 340 345 350
 Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
 355 360

<210> 23

<211> 861

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

<400> 23

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 aaacatgagt gtcatttctt caacgggacg gagcggtgac ggttcctgga cagatacttc 180
 tatcaccaag aggagtacgt gcgcttcgac agcgacgtgg gggagtaccg ggcgggtgacg 240

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gagctggggc ggctgatgc cgagtactgg aacagccaga aggacctcct ggagcagaag 300
cgggcccggg tggacaccta ctgcagacac aactacgggg ttggtgagag cttcacagtg 360
cagcggcgag tctatcctga ggtgactgtg tatcctgcaa agaccagcc cctgcagcac 420
cacaacctcc tggctctgctc tgtgaatggt ttctatccag gcagcattga agtcagggtg 480
ttccggaacg gccaggaaga gaagactggg gtggtgtcca caggcctgat ccagaatgga 540
gactggacct tccagaccct ggtgatgctg gaaacagttc ctcggagtgg agaggtttac 600
acctgccaag tggagcacc cagcctgacg agccctctca cagtggaatg gagagcacgg 660
tctgaatctg cacagagcaa gggcggctcc ggtggtagcg cccagctgaa gaagaaactc 720
caggctctga aaaaaaagaa tgcccagctc aagcagaagc tgcaggccct gaagaaaaag 780
ctggctcagg gttccgggtg ttccgcggtt ggtggtttga acgacatctt cgaagctcag 840
aaaatcgaat ggcactaata a 861

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<210> 24

<211> 285

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

<400> 24

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Met Val Cys Leu Lys Phe Pro Gly Gly Ser Cys Met Ala Ala Leu Thr
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Val Thr Leu Met Val Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr
          20          25          30
Arg Pro Arg Phe Leu Glu Gln Val Lys His Glu Cys His Phe Phe Asn
          35          40          45
Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr His Gln Glu
          50          55          60
Glu Tyr Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr
65          70          75          80
Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu
          85          90          95
Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr
          100         105         110
Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val
          115         120         125
Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu
          130         135         140
Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp
145         150         155         160
Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser Thr Gly Leu
          165         170         175
Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr
          180         185         190
Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser
          195         200         205
Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala
          210         215         220
Gln Ser Lys Gly Gly Ser Gly Gly Ser Ala Gln Leu Lys Lys Lys Leu
225         230         235         240
Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala
          245         250         255
Leu Lys Lys Lys Leu Ala Gln Gly Ser Gly Gly Ser Ala Gly Gly Gly
          260         265         270
Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His
          275         280         285

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09756983 010501